

An African swine fever virus genotype present in both the resistant bushpig (*Potamochoerus larvatus*) and adjacent domestic pig populations does not induce detectable clinical ASF symptoms

Okoth, E.A.¹, Macharia, J.M.², Omere, A.¹, Pelayo, V.³, Bulimo, W.⁴, Arias, M.³, Kitala, P.⁴, Lekolol, I.⁵, Mijele, D.⁵ and Bishop, R.P.¹, ¹International Livestock Research Institute (ILRI), Kenya, ²Department of Veterinary Services, Ministry of livestock Development, Kenya, ³Centro de Investigación en Sanidad Animal (CISA-INIA), Spain, ⁴University of Nairobi, Kenya, ⁵Department of Wildlife Services, Ministry of Tourism and Wildlife, Kenya; e.okoth@cgiar.org

The role of the bushpig in the transmission of the African swine fever virus (ASFV) to domestic pigs remains little understood. We describe a study conducted in Homabay district in Western Kenya in which free range-low input pig management system was characterized in relation to potential risk of ASFV infection posed by bushpigs. A questionnaire was used to collect information from 81 randomly selected pig-rearing households. Blood was collected from 179 domestic pigs. Also, 8 Bushpigs were sampled from Ruma National Park that neighbour the same study area, 8 for blood and 1 for tissues. The samples were analyzed using OIE serological and nucleic acid-based prescribed diagnostic techniques. The household survey showed all farms practiced free range/tethering feed management. The animals exhibited inapparent African swine fever and farmers had not observed the disease. The PCR assay of blood based on the p72 gene primers demonstrated 22% positivity to ASFV, but no animals were sero-positive by the OIE indirect ELISA. One of the 8 bushpigs sampled was PCR positive in Kidney tissue. Dendrograms based on the sequence of the C-terminal end of the p72 gene and the full-length p54-gene of domestic pig and bushpig ASFV viruses indicated that the domestic and bushpig viruses clustered together genetically. Similarly, the predicted amino acid sequence of the tetrameric repeats that constitute the central variable region of the B602L gene also exhibited a high degree of identity. These results suggest a common source of infection or viral transmission between the two pig species.